Figure 1.

i n			ī/4		
to usage i					
ation to				·	
in rel					
frequencies					
wing codon	Ser	UCC 0.37 UCU 0.34 AGC 0.20 UCG 0.04 AGU 0.03	158		
ro and show	Gln	CAG 0.86 CAA 0.14 L			
(a) Nucleotide sequences for Ala-Ile-Lys-Leu-Val-Gln-Ser-Pro and showing codon frequencies in relation enteric bacterial genes	Val	GUU 0.51 GUA 0.26 GUG 0.16 GUC 0.07	125		
lle-Lys-Leu-V	Leu	CUG 0.83 CUC 0.07 CUU 0.04 UUG 0.03 UUA 0.02	135		
es for Ala-1 s	Lys	AAA 0.74 AAG 0.26	269		
de sequence erial genee	Ile	AUC 0.83 AUU 0.17 AUA 0.00	260		
(a) Nucleotide sequences enteric bacterial genes	Ala	GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10	178	8 Pro	CCG 0.77 CCA 0.15 CCU 0.08
•					

and showing codon						
lla-Ile-Lys-Leu-Val-Gln-Ser-Pro-Asn-Gly-Asn-Phe-Ala-Ala-Ser ige in enteric bacterial genes	Ser	C 0 .37 C 0 .20 G 0 .04 U 0 .03	Ala	U 0,35 A 0,28 G 0,26 C 0,10		
n-Gly-A		86 UCC 14 UCU AGC UCG AGU UCG	1	0.35 GCU 0.28 GCA 0.26 GCG 0.10 GCC		
:-Pro-As mes	Gln	CAG 0.86 CAA 0.14	Ala	GCU 0. GCA 0. GCG 0. GCC 0.		
-Val-Gln-Ser pacterial ge	Val	GUU 0.51 GUA 0.26 GUG 0.16 GUC 0.07	Phe	UUC 0.76 UUU 0.24 34		
Ile-Lys-Leu in enteric }	Leu	CUG 0.83 CUC 0.07 CUU 0.04 UUG 0.03 UUA 0.02 CUA 0.00	Asn	AAC 0.94 AAU 0.06 88		
sequences for Ala- relation to usage	Lys	AAA 0.74 AAG 0.26	Gly	GGU 0.59 GGC 0.38 GGG 0.02 GGA 0.00		
le sequence n relation	Ile	AUC 0.83 AUU 0.17 AUA 0.00	Asn	AAC 0.94 AAU 0.06 396		
(b) Nucleotide frequencies in	Ala	GCU 0.35 GCA 0.28 GCG 0.26 GCC 0.10	. 8 . 14 Pro	CCG 0.77 CCA 0.15 CCU 0.08 CCC 0.00	15 Ser	UCC 0.37 UCU 0.34 AGC 0.20 UCG 0.04 AGU 0.03 UCA 0.03

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Thr- genes																								
al-Leu-Asp-Gly- eric bacterial																								
(c)Nucleotide sequences for Ala-Ile-Lys-Leu-Val-Gln-Ser-Pro-Asn-Gly-Asn-Phe-Ala-Ala-Ser-Phe-Val-Leu-Asp-Gly-Thr- Lys-Trp-Ile-Phe-Lys-Ser-Lys-Tyr-Tyr and showing codon frequencies in relation to usage in enteric bacterial gene																								
y-Asn-Phe-Ala in relation t	Ser	UCC 0.37		AGC 0.20	UCG 0.04		UCA 0.02	158		Ala	GCU 0.35	GCA 0.28	GCG 0.26	GCC 0.10	50		Thr	ACC 0.55	ACU 0.35	ACG 0.07	ACA 0.04		,	338
-Pro-Asn-Glyrequencies	Gln	CAG 0.86	CAA 0.14					230		Ala		GCA 0.28	GCG 0.26		34		Glγ	GGU 0.59	GGC 0.38	GGG 0.02	GGA 0.00	•	,	240
Val-Gln-Ser ing codon fi	Val	GUU 0.51			GUC 0.07			125		Phe	UUC 0.76	UUU 0.24			34		Asp	GAC 0.67	GAU 0.33				,	161
le-Lys-Leu-Vr and show:	Leu	CUG 0.83	CUC 0.07	CUU 0.04	UUG 0.03	UUA 0.02	CUA 0.00	135		Asn	AAC 0.94	AAU 0.06			88		ren	CUG 0.83		CUU 0.04	UUG 0.03	UUA 0.02		180
s for Ala-I) :-Lys-Tyr-Ty	Lys	AAA 0.74	AAG 0.26					269		Gly	GGU 0.59	GGC 0.38		GGA 0.00	148		Val	GUU 0.51		GUG 0.16			,	167
e sequences Phe-Lys-Ser	ile	AUC 0.83	AUU 0.17	AUA 0.00				260		Asn	AAC 0.94	AAU 0.06			396		Phe	UUC 0.76	UUU 0.24				,	216
(c)Nucleotide sequences for Ala-Ile Lys-Trp-Ile-Phe-Lys-Ser-Lys-Tyr-Tyr	Ala	GCU 0.35	GCA 0.28	GCG 0.26	GCC 0.10			178	8 . 14	o H	CCG 0.77		CCU 0.08	CCC 0.00	401	15 - 21	Ser			AGC 0.20			UCA 0.02	119

Lys	Trp	Ile	Phe	Lys	Ser	Lys
AAA 0.74 AAG 0.26	UGG 1.00	AUC 0.83 AUU 0.17 AUA 0.00	UUC 0.76 UUU 0.24	AAA 0.74 AAG 0.26	UCC 0.37 UCU 0.34 AGC 0.20	AAA 0.74 AAG 0.26
					UCG 0.04 AGU 0.03 UCA 0.02	
467	467	173	154	152	154	0
29 - 30 Tyr	Tyr					
UAC 0.75 UAU 0.25	UAC 0.75 UAU 0.25					
0	0					